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A success for community science: *Carmenta brachyclados* sp. nov. (Lepidoptera, Sesiidae, Synanthedonini), a clearwing moth from Guyana discovered with its hostplant indoors in Wales (United Kingdom)

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Abstract. A new species of Sesiidae, *Carmenta brachyclados* Sterling & Lees, 2024 is described from adult specimens, pupal exuviae and larval borings which were accidentally transported to South Wales, United Kingdom. DNA barcoding and morphological evidence shows that this species is native to the Neotropics, where it feeds in the seedpods of the leguminous tree, *Mora excelsa* Benth. (Fabaceae: Caesalpinioideae) and that it is related to a group of seed-feeding species of clearwing moths within the genus *Carmenta* Edwards, 1881, naturally occurring in the Neotropics and southern Nearctic, although *C. mimosa* Eichlin & Passoa, 1984 has been introduced in Australia and elsewhere as a biological agent.

Whilst in Guyana, local people told my mother, Ashleigh Cadet,
that if she left an offering of tobacco to the jungle spirits, she would be shown
something beautiful from the jungle, so that is what she did - DTC.

Introduction

Ashleigh Cadet, a professional photographer and the mother of DTC, lives in Port Talbot, South Wales. Port Talbot is more famous in the United Kingdom for its steelworks than its clearwing moths. However, on 4 February 2024 DTC (who is not a lepidopterist) spotted an insect flying at a window in the house which she shares with Ashleigh. On closer inspection there was a similar but dead specimen on the windowsill. DTC posted an image of the live specimen on Instagram (Fig. 1). This post was seen by Graeme Davis, a knowledgeable amateur UK lepidopterist, who considered that this was not a species previously recorded in the UK. Graeme forwarded the post to Les Evans-Hill, the data officer for Butterfly Conservation, the principal UK charity for the conservation of butterflies and moths. Les contacted MJS for confirmation of Graeme's (and his) view, asked MJS to provide an identity for the specimens and put DTC in contact with the Natural History Museum, London (NHMUK).

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As DTC had found a live specimen, MJS and DCL sent DTC some images of larval workings and pupal exuviae of clearwing moths and suggested she search the plants in the house. Unknown to MJS and DCL, this was no mean task as both DTC and Ashleigh are keen plant growers, but a careful search and identification of some 85 living indoor pot plants and any remaining cut flowers which could be found produced no obvious sesiid hostplants and no exuviae. The live specimen had died in the fridge, but DTC brought both specimens, still in good condition, to the NHMUK for identification. Both specimens were promptly DNA barcoded by the third author (JB). The results suggested that they belonged to the genus *Carmenta* Edwards, 1881, a large genus of Sesiidae distributed throughout the Americas and that they belonged to an apparently seed boring group from central America/the northern part of South America.

This finding was a lightbulb moment. Ashleigh had returned (on 18 October 2023) from a photographic assignment in Guyana. In a corner of the room in which the specimens had been found lay Ashleigh's boot bag, back from the trip. DTC carefully searched the boot bag and in debris and dried mud at its bottom found two pupal exuviae, both almost intact (Figs 2, 3), and some fragments of plant material. The fragments were tiny but the largest fragment (which DTC scraped clean of mud), even though it was only the size of a 50p piece (Fig. 4), had two holes which were almost the same diameter as the pupal exuviae, and galleries and frass mixed with silk (Figs 5, 6).

The fragment and the exuviae were carefully preserved by DTC and sent to the NHMUK. Examination of two potentially still capped tunnels revealed nothing more inside. The fragment was shown by DCL and MJS to Dr Sandra Knapp (NHMUK) who immediately suggested that it was part of a seedpod and even suggested a genus for it (correctly as it proved). This raised the possibility that the plant fragment could itself be identified by DNA barcoding using plant primers.

Carmenta is a genus which is almost exclusively known from the Americas. This paper represents what appears to be the first record of the genus *Carmenta* from Europe or the UK (albeit accidentally imported without release into the wild). Outside the Americas, the genus is known from Australia, Indonesia, Malaysia, Thailand, Vietnam and Hawaii, where *Carmenta mimosa* Eichlin & Passoa, 1984 has been introduced as a biological control for the invasive leguminous weed, *Mimosa pigra* L. (Paynter, 2005). In Central and South America a few species of *Carmenta* have pest status, notably *C. foraseminis* Eichlin, 1995 which infests cocoa pods (*Theobroma cacao* L.) (Harms and Aiello 1997; Delgado et al. 2023), and *C. theobromae* Busck, 1910 (a species also reported as a pest of Guava *Psidium guajava* L.; Pulido-Blanco et al. 2010).

Taft and Cognato (2017) analysed COI for 36 species of *Carmenta* when recognising a new species, *C. wildishorum* Taft & Cognato, 2017, so this study provides us an opportunity to enlarge on their results. Cognato et al. (2022) further provided a multigene phylogeny including some representatives of *Carmenta* and others of the tribe Synanthedonini which showed *Alcathoe* Edwards, 1882, *Hymenoclea* Engelhardt, 1946, and *Penstemonia* Engelhardt, 1946 all fall within *Carmenta*, suggesting that the genus is polyphyletic as currently constituted.

The present description of a new species follows a comparison by the naming authors of the specimens to the described species of *Carmenta* and to other sesiid materials at the NHMUK and on BOLD.

Materials and methods

The adult specimens of the new taxon belonging to Sesiidae (hereafter 'the mystery clearwing') were obtained indoors in South Wales. The mystery clearwing specimens were relaxed in a chamber containing water and a few drops of glacial acetic acid and set at the NHMUK,

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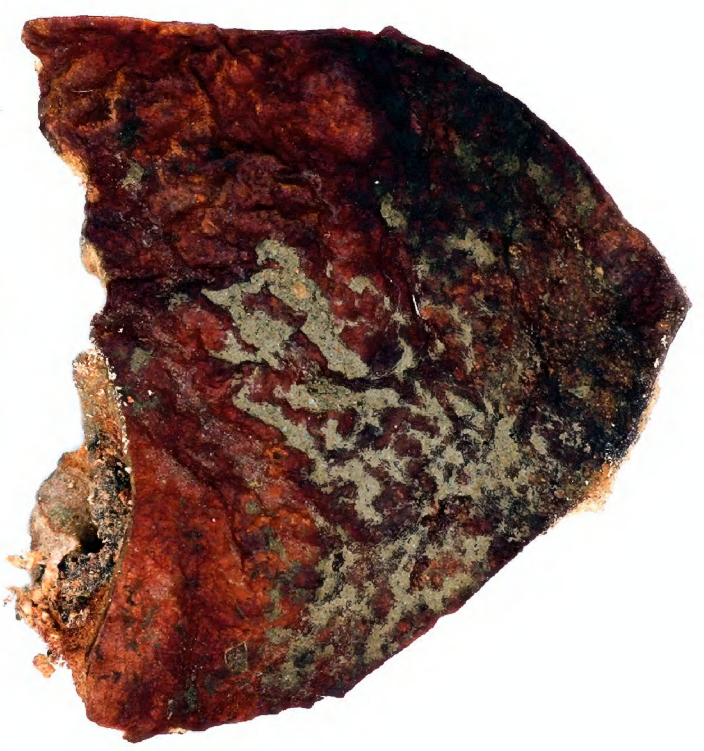

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Figures 1–6. *Carmenta brachyclados* sp. nov. **1.** Holotype ♀ habitus; **2.** Pupal exuvium dorsal, NHMUK013700485; **3.** Pupal exuvium latero-ventral, NHMUK013700485; **4.** Fragment of seedpod of *Mora excelsa*, NHMUK013700486; **5, 6.** Parts of fragment of seedpod showing exit holes and larval workings.

after legs had been removed from each specimen for DNA barcoding. They were then compared to the collection of Sesiidae at the NHMUK (including supplementary collections and accessions). In addition, following the results of DNA barcoding, which showed that almost all the specimens identified to species level in the top 99 hits in the BOLD identification engine (https://boldsystems.org/index.php/IDS_OpenIdEngine) were species of the genus *Carmenta*, the mystery clearwing was also compared to all described species currently placed in *Carmenta*. A checklist of these described species was prepared from Pühringer and Kallies (2004), which was updated through internet searches for species of *Carmenta* described since 2004. An initial comparison was made between the external morphology of the mystery clearwing specimens and the sesiids in the NHMUK collection and images of those species of *Carmenta* not represented in the NHMUK collection. This enabled many species to be ruled out as possible identities for the mystery sesiid species. A shortlist was then drawn up of species (all *Carmenta*) for which more detailed morphological analysis was required in order to determine whether the mystery clearwing specimens were examples of one of these species. The species reviewed in detail were: *C. deipyla* (Druce, 1883), *C. benoisti* (Le Cerf, 1917), *C. whitelyi* (Druce, 1889), *C. guatemalena* (Druce, 1883), *C. flavostrigata* (Le Cerf, 1917), *C. foraseminis* Eichlin, 1995, *C. guyanensis* (Le Cerf, 1917), *C. surinamensis* (Möschler, 1878), *C. theobromae* (Busck, 1910), *Carmenta* cf. *whitelyi* and *Carmenta* sp. lep.131.

For these species, the original description was located and compared to the mystery clearwing. Type specimens and (if dissected) their genitalia were examined if these were held at the NHMUK. In other cases, an image (of the type (female allotype or syntype where possible) was also compared to the mystery clearwing. The genitalia of two female specimens of *Carmenta* cf. *whitelyi* were compared to those of one of the mystery clearwings (slide number NHMUK014332461) and, in the case of *C. theobromae*, a non-type specimen and images of further non-types were compared.

The process for comparing the mystery clearwing to the shortlisted *Carmenta* species is set out in Suppl. material 1.

Initial query, neighbor joining tree and phylogenetics of the sesiid

The two sequences from the two sesiid specimens are identical. One of the sequences (for NHMUK013700463) was queried on BOLD (on 23/02/2024). A neighbor joining (NJ) tree was constructed, and minimum p-distances were calculated between the query sequence and nearest neighbours using 100-Identity. We then downloaded all available BINs identified as *Carmenta* with GenBank accessions from BOLD (on 5/05/2024), together with those identified as *Alcathoe*, *Hymenoclea*, and *Penstemonia* (following the results of the phylogenetic analysis of Cognato et al. (2023)) and ran the query sequence with them using default options in Phyml 3.0 (online; http://www.atgc-montpellier.fr/phyml/execution.php), including the model selected by Bayesian Information Criterion (GTR + R model favoured) and ABayes support.

Morphological identity, initial query, neighbor joining tree and phylogenetics of the plant fragment

The fragment of plant material was shown to Dr. Sandra Knapp for an approximate identification, and she immediately suggested part of the seedpod of the legume genus *Mora* R.H. Schomb. ex Benth. (1839). DNA barcode sequences were subsequently extracted as follows.

Methodology of plant fragment preparation and sequencing conditions, bioinformatics.

A small fragment (<1 cm) of seed was prepared for extraction by grinding in liquid nitrogen with a pestle and mortar. Half of the resulting powder was then used for DNA extraction with a cetyltrimethylammonium bromide (CTAB) extraction (DOI: https://dx.doi.org/10.17504/protocols.io.e6nvw157zlmk/v1). Purified DNA was quantified by nanodrop. Three regions were used to generate DNA barcodes, rbcL, matK and ITS2 (Table 1). Plant DNA barcoding markers amplified the following fragment lengths: MatK (686 bp), rbcL (550 bp), and ITS2 (322 bp).

Table 1. Primer sequences for seed DNA barcoding.

DNA barcoding region	Primer name	Sequence 5'–3'
ITS2	ITS3	GCATCGATGAAGAACGCAGC
	ITS4	TCCTCCGCTTATTGATATGC
MatK	MatK_1R_kim	ACCCAGTCCATCTGGAAATCTTGGTCC
	MatK-3FKIM-r	CGTACAGTACTTTTGTGTTTACGAG
rbcL	rbcLa-F	ATGTCACCACAAACAGAGACTAAAGC
	rbcLa-R	GTAAAATCAAGTCCACCRCG

PCRs were performed using the KAPA Plant PCR kit in 25 µl reaction volumes comprising 12.5 µl KAPA Plant PCR buffer, 4.8 µl nuclease free water, 1 µl 25 mM MgCl2, 0.75 µl 10 µM forward primer, 0.75 µl 10 µM reverse primer, 0.2 µl polymerase and 5 µl DNA template. The following thermocycling protocol was used: 20 s at 95 °C for initial denaturation, followed by 35 cycles of 20 s at 95 °C for denaturation, 15 s at 55 °C for annealing, 20 s at 72 °C for extension, and 1 min at 72 °C for the final extension. PCR amplicons were visualised on a 1% agarose gel and quantified by Qubit. Amplicons were pooled for library preparation with the Oxford Nanopore Ligation Sequencing kit (v14) and sequenced on a Flongle (v10.4.1). Resulting reads were aligned and consensus sequences generated using Geneious (v2023.0.4). For MatK, the final sequence was a consensus of 393 fragments; for rbcL, 259; and for ITS2, 100.

We used Phyml 3.0 (online) to run the final query sequences (MatK, 686 bp; rbcL, 599 bp) as part of an alignment including all genera found in the Bruneau et al. (2024) caesalpinioid phylogeny for their tribe Dimorphandreae, namely *Dimorphandra*, *Burkea*, *Stachyothyrsis* and *Mora*, with representative species downloaded from GenBank (on 1/05/2024)

The illustrated material, other than Fig. 1, was photographed using a Canon EOS 5DSR camera and MP-E 65 mm lens equipped with a Stackshot system operated by Helicon Remote software (version 3.8.4 W); the shots were eventually stacked with Helicon Focus software (version 6.7.1), which was set up with montage controlled by Helicon using a motorised deck in about 30 to 40 steps for adults and 10 to 15 steps for genitalia and wing preparations. Fig. 1 was photographed on an iPhone 8 using an Apexel 12× Macro Lens.

Description of the external features of the new taxon follows Špatenka et al. (1999), and of genitalia follows Eichlin and Duckworth (1988). DNA barcodes for the moth and plant specimens are publicly available on BOLD (http://v4.boldsystems.org/index.php/MAS_Management_DataConsole?codes=DS-CARMENTA) with Project IDs UKMOT014-24 (NHMUK013700462) and Process ID UKMOT015-24 (NHMUK013700463) and GenBank accession numbers (COI-5P) PP866044 and PP866043 respectively and the plant accession codes for seedpod fragment(s) NHMUK013700486 are: MatK: PP872149; rbcL: PP872150 and fungal accession code for ITS2: PP840606.

Accession numbers and other data for sequences used in all trees (Figs 7–10) are summarized in Suppl. material 2.

Results

Molecular results

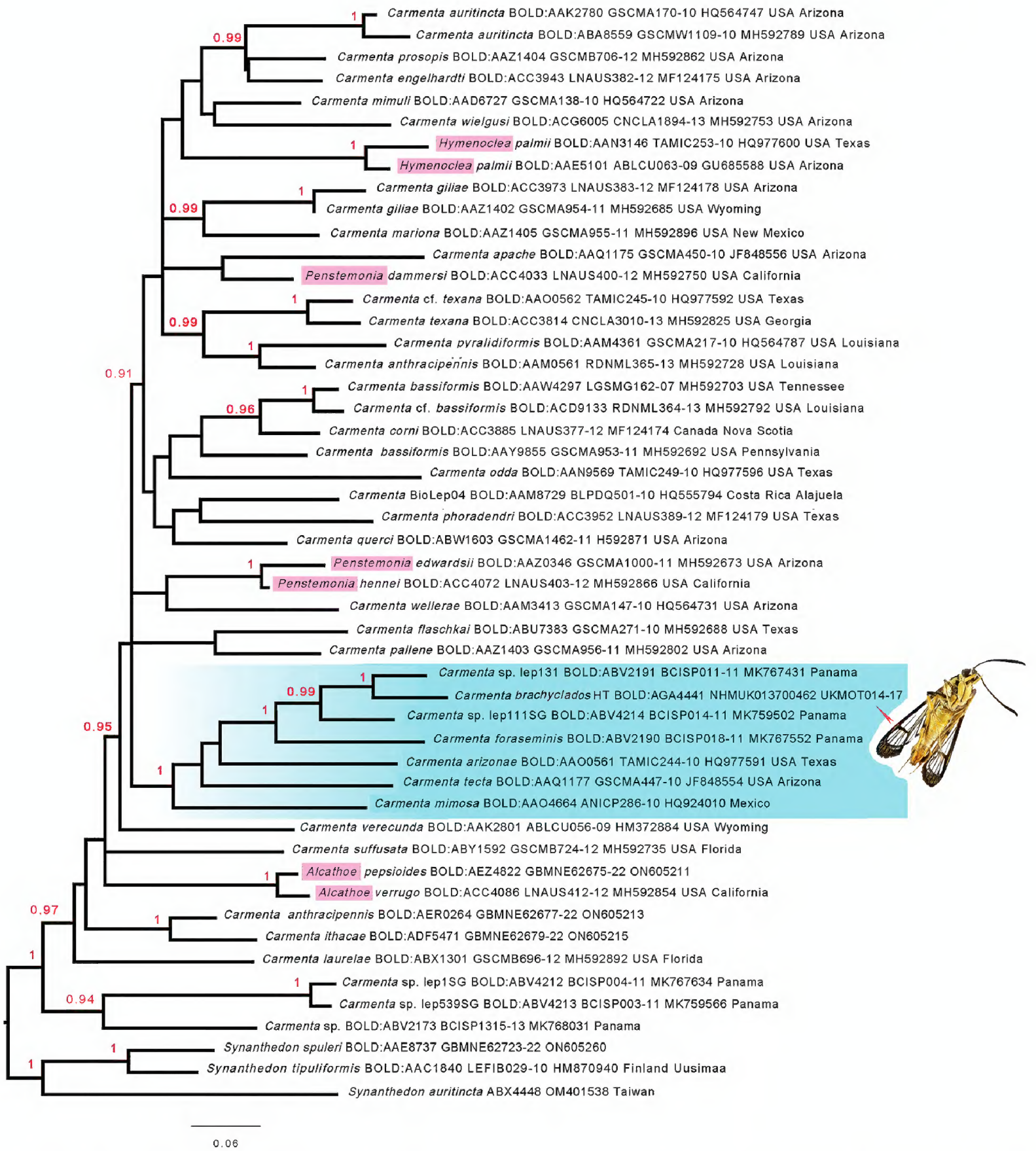
The initial query of the mystery clearwing (NHMUK013700462) on BOLD resulted in a 5.66% p-distance to the nearest hit ("*Carmenta* sp. lep131", representing Barcode Index Cluster [BIN] BOLD:ABV2191). Only DNA barcodes identified as the genus *Carmenta* appeared in the top 50 hits with a maximum of 10.4% p-distance. In all there were 244 sequences identified to the genus *Carmenta* representing 52 identified species with 72 BINs publicly available on BOLD (on 16/08/2024). Following branching patterns in the resulting NJ tree, NHMUK01370046 was 6.57% p-distant to both *C. guyanensis* from French Guiana (BOLD:AAM7091) and a species from Costa Rica (BOLD:AEF7752), 7.07% p-distant to another species from Costa Rica (BOLD:AET8297), 7.34% p-distant to sp. lep111SG from Panama (BOLD:ABV4214), 8.97–9.22% p-distant to BOLD:AAK2798 (variously identified as *C. surinamensis*, *C. foraseminis* and *C. theobromae*), and 10.09–10.22% p-distant to *C. foraseminis* (BOLD:ABV2190).

The mystery clearwing clearly fitted with the genus *Carmenta* from a DNA barcode perspective (Fig. 7). Running the sequence (for NHMUK013700463) with the other 40 representatives of single BINs of the genus on BOLD plus eight representatives from *Penstemonia*, *Alcathoe* and *Hymenoclea* that had GenBank accession numbers on Phyml 3.0 (online) resulted in it falling within a clade (pp = 1) subtended by *C. mimosae* and including also *C. tecta* (Edwards, 1882) and *C. arizonae* (Beutenmüller, 1898) and in a subclade that included *C. foraseminis* and two apparently undescribed species from Barro Colorado Island, Panama (BINs, BOLD:ABV4214 and BOLD: ABV2191), with an apparent sister relationship to the latter.

Adding in available BIN cluster representatives downloaded from BOLD (on 5/05/2024) and running again in Phyml 3.0 (online) resulted in Fig. 8 in which the mystery clearwing belonged to a clade (pp = 1) with exemplars identified on BOLD as follows: *C. surinamensis* from French Guiana (BOLD: AAK2798), two specimens of *C. foraseminis* from Panama, reared respectively from *Gustavia superba* (H.B. Kunth) O. Berg (Lecythidaceae) and *Lafoensia punicifolia* DC (Lythraceae) (BOLD: ABV2190) (these also form a sub-clade (pp = 1); and *Carmenta* sp. lep111SG from Panama, reared from *Prioria copaifera* Griseb., Fabaceae (BOLD: ABV4214), *Carmenta* sp. lep131 from Panama, reared from *Strychnos panamensis* Seem. (Loganiaceae) (BOLD: ABV2191) and *C. guyanensis* from French Guiana (BOLD:AAM7094) (these latter exemplars forming a sub-marginally supported grouping (pp = 0.94) with the DNA barcode of the mystery sesiid).

For the plant DNA barcodes, Blast results (https://blast.ncbi.nlm.nih.gov/Blast.cgi) for the seedpod fragments Matk showed a perfect match of 100% with *Mora excelsa* Benth. (KX538501), a 99.71% match with *M. gonggrijpii* (Kleinhoonte) Sandwith (KX538485, EU362005), a 98.98% match with *Stachyothyrsus staudtii* Harms (JX099332), and a 98.69% match to *Dimorphandra conjugata* (Splitg.) Sandwith (EU361934).

The Phyml tree for the Matk marker (Fig. 9) shows a fit within the genus *Mora* (pp = 1) (excluding *M. oleifera* (PP449167)) and a perfect match to an exemplar of *Mora excelsa* (KX538501). The rbcL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Carmenta auritincta BOLD:ABA8559 GSCMW1109-10 MH592789 USA Arizona
Carmenta prosopis BOLD:AAZ1404 GSCMB706-12 MH592862 USA Arizona
Carmenta engelhardti BOLD:ACC3943 LNAUS382-12 MF124175 USA Arizona
Carmenta mimuli BOLD:AAD6727 GSCMA138-10 HQ564722 USA Arizona
Carmenta wielgusi BOLD:ACG6005 CNCLA1894-13 MH592753 USA Arizona
Hymenoclea palmii BOLD:AAN3146 TAMIC253-10 HQ977600 USA Texas
Hymenoclea palmii BOLD:AAE5101 ABLCU063-09 GU685588 USA Arizona
Carmenta giliae BOLD:ACC3973 LNAUS383-12 MF124178 USA Arizona
Carmenta giliae BOLD:AAZ1402 GSCMA954-11 MH592685 USA Wyoming
Carmenta mariona BOLD:AAZ1405 GSCMA955-11 MH592896 USA New Mexico
Carmenta apache BOLD:AAQ1175 GSCMA450-10 JF848556 USA Arizona
Penstemonia dammersi BOLD:ACC4033 LNAUS400-12 MH592750 USA California
Carmenta cf. texana BOLD:AAO0562 TAMIC245-10 HQ977592 USA Texas
Carmenta texana BOLD:ACC3814 CNCLA3010-13 MH592825 USA Georgia
Carmenta pyralidiformis BOLD:AAM4361 GSCMA217-10 HQ564787 USA Louisiana
Carmenta anthracipennis BOLD:AAM0561 RDNML365-13 MH592728 USA Louisiana
Carmenta bassiformis BOLD:AAW4297 LGSMG162-07 MH592703 USA Tennessee
Carmenta cf. bassiformis BOLD:ACD9133 RDNML364-13 MH592792 USA Louisiana
Carmenta corni BOLD:ACC3885 LNAUS377-12 MF124174 Canada Nova Scotia
Carmenta bassiformis BOLD:AAY9855 GSCMA953-11 MH592692 USA Pennsylvania
Carmenta odda BOLD:AAN9569 TAMIC249-10 HQ977596 USA Texas
Carmenta BioLep04 BOLD:AAM8729 BLPDQ501-10 HQ555794 Costa Rica Alajuela
Carmenta phoradendri BOLD:ACC3952 LNAUS389-12 MF124179 USA Texas
Carmenta querci BOLD:ABW1603 GSCMA1462-11 H592871 USA Arizona
Penstemonia edwardsii BOLD:AAZ0346 GSCMA1000-11 MH592673 USA Arizona
Penstemonia hennei BOLD:ACC4072 LNAUS403-12 MH592866 USA California
Carmenta wellerae BOLD:AAM3413 GSCMA147-10 HQ564731 USA Arizona
Carmenta flaschkai BOLD:ABU7383 GSCMA271-10 MH592688 USA Texas
Carmenta pallene BOLD:AAZ1403 GSCMA956-11 MH592802 USA Arizona
Carmenta sp. lep131 BOLD:ABV2191 BCISP011-11 MK767431 Panama
Carmenta brachyclados HT BOLD:AGA4441 NHMUK013700462 UKMOT014-17
Carmenta sp. lep111SG BOLD:ABV4214 BCISP014-11 MK759502 Panama
Carmenta foraseminis BOLD:ABV2190 BCISP018-11 MK767552 Panama
Carmenta arizonae BOLD:AAO0561 TAMIC244-10 HQ977591 USA Texas
Carmenta tecta BOLD:AAQ1177 GSCMA447-10 JF848554 USA Arizona
Carmenta mimosa BOLD:AAO4664 ANICP286-10 HQ924010 Mexico
Carmenta verecunda BOLD:AAK2801 ABLCU056-09 HM372884 USA Wyoming
Carmenta suffusata BOLD:ABY1592 GSCMB724-12 MH592735 USA Florida
Alcathoe pepsioides BOLD:AEZ4822 GBMNE62675-22 ON605211
Alcathoe verrugo BOLD:ACC4086 LNAUS412-12 MH592854 USA California
Carmenta anthracipennis BOLD:AER0264 GBMNE62677-22 ON605213
Carmenta ithacae BOLD:ADF5471 GBMNE62679-22 ON605215
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Carmenta sp. lep1SG BOLD:ABV4212 BCISP004-11 MK767634 Panama
Carmenta sp. lep539SG BOLD:ABV4213 BCISP003-11 MK759566 Panama
Carmenta sp. BOLD:ABV2173 BCISP1315-13 MK768031 Panama
Synanthedon spuleri BOLD:AAE8737 GBMNE62723-22 ON605260
Synanthedon tipuliformis BOLD:AAC1840 LEFIB029-10 HM870940 Finland Uusimaa
Synanthedon auritincta ABX4448 OM401538 Taiwan
0.06

Figure 7. Phylogenetic tree using Phyml 3.0 of the DNA barcode of the holotype of the new taxon (NHMUK013700462) run with DNA barcodes of representative BIN clusters for the other 40 publicly available BINs of *Carmenta* spp. Supports shown on nodes are ABayes measure in Phyml 3.0 (see Methods), with a minimum of 0.95 being considered significant for the purposes of this analysis. The clade subtended by *C. mimosa*, which includes the new taxon, is highlighted in light blue. The tree was rooted in FigTree using three representatives of the genus *Synanthedon* including the type species *S. tipuliformis* and publicly available BINS of three other genera (*Hymenocloa*, *Penstemonia* and *Alcathoe*, highlighted in pink) likely to be internal to *Carmenta* (see Methods). The accompanying image is the ventral surface of the holotype of the new taxon prior to relaxing and setting.

marker showed a more equivocal result with a 100% Blast match with both *M. excelsa* (MF786347) and *Stachyothyrsus stapfiana* (MN366716) and a few nucleotides difference to *Burkea africana* (KX119267); no sequence for *M. gonggrijpii* was available for this marker (these results are reflected by the Phyml 3.0 run in Fig. 10, in which these exemplars comprise a clade (pp = 0.998)). The results of both these markers are consistent with *Mora excelsa* being the correct identity of the plant fragment. The ITS marker failed to match the identity of the hostplant tree, whilst it produced matches with species of the fungal genus *Talaromyces* R.Benj. (1955), Trichocomaceae (e.g. 93.79% identity to MT528976).

Morphological results

The generic characters for *Carmenta* are: ductus bursae sclerotized on at least ½ its length for most species; ductus seminalis arising midway between posterior end and corpus bursae or nearer the latter in most species; most species without signum on corpus bursae (Eichlin and Duckworth 1988). The female genitalia of the mystery clearwing taxon are typical for *Carmenta* spp.

The morphological results at the specific level are set out in Suppl. material 1 and summarised here. There are substantial differences between characters described in the original

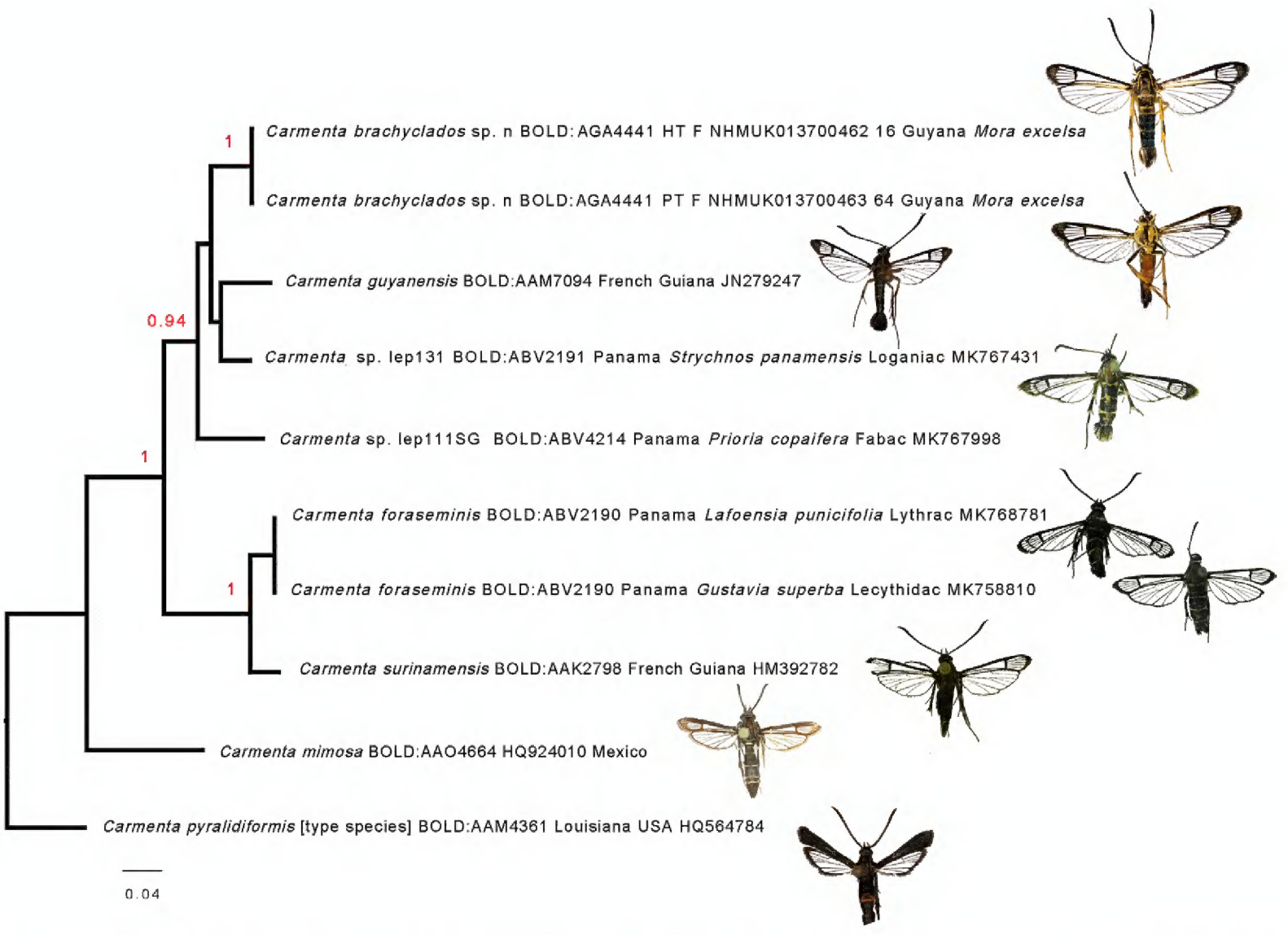
1
Carmenta brachyclados sp. n BOLD:AGA4441 HT F NHMUK013700462 16 Guyana Mora excelsa
Carmenta brachyclados sp. n BOLD:AGA4441 PT F NHMUK013700463 64 Guyana Mora excelsa
Carmenta guyanensis BOLD:AAM7094 French Guiana JN279247
0.94
Carmenta sp. lep131 BOLD:ABV2191 Panama Strychnos panamensis Loganiac MK767431
Carmenta sp. lep111SG BOLD:ABV4214 Panama Prioria copaifera Fabac MK767998
1
Carmenta foraseminis BOLD:ABV2190 Panama Lafoensia punicifolia Lythrac MK768781
1
Carmenta foraseminis BOLD:ABV2190 Panama Gustavia superba Lecythidac MK758810
Carmenta surinamensis BOLD:AAK2798 French Guiana HM392782
Carmenta mimosa BOLD:AAO4664 HQ924010 Mexico
Carmenta pyralidiformis [type species] BOLD:AAM4361 Louisiana USA HQ564784
0.04

Figure 8. Phylogenetic tree using Phyml 3.0 showing the position of the DNA barcode of the holotype of the new taxon (NHMUK013700462) in the context of likely seed-boring Neotropical sesiids and focusing on host associations, which are a subclade of the light blue highlighted clade in Fig. 7, rooted in FigTree with the type species of *Carmenta*, *C. pyralidiformis*. Additional DNA barcodes are included for *C. guyanensis*, *C. surinamensis*, and different hostplant rearings for *C. foraseminis*. *C. brachyclados* (holotype and paratype sequences are identical) are part of a clade of at least four Neotropical species.

descriptions of all the shortlisted taxa and the corresponding characters of the mystery clearwing species. In addition, for *C. deipyla* and *C. guatemalena*, there are differences both in the external appearance of the types (females in each case) and in the shape of the ductus bursae of the genitalia of the types compared to that of the mystery clearwing. For *C. foraseminis* and *C. guyanensis*, the external appearance of the allotype of the former and the type of the latter is different from the mystery clearwing. Also, the DNA barcodes of the former (BIN, BOLD:ABV2190) and the latter (BIN, BOLD:AAM7094) were, respectively, 10.09% and 6.57% divergent from the DNA barcode for the unknown specimens (BIN, BOLD:AGA4441); see above.

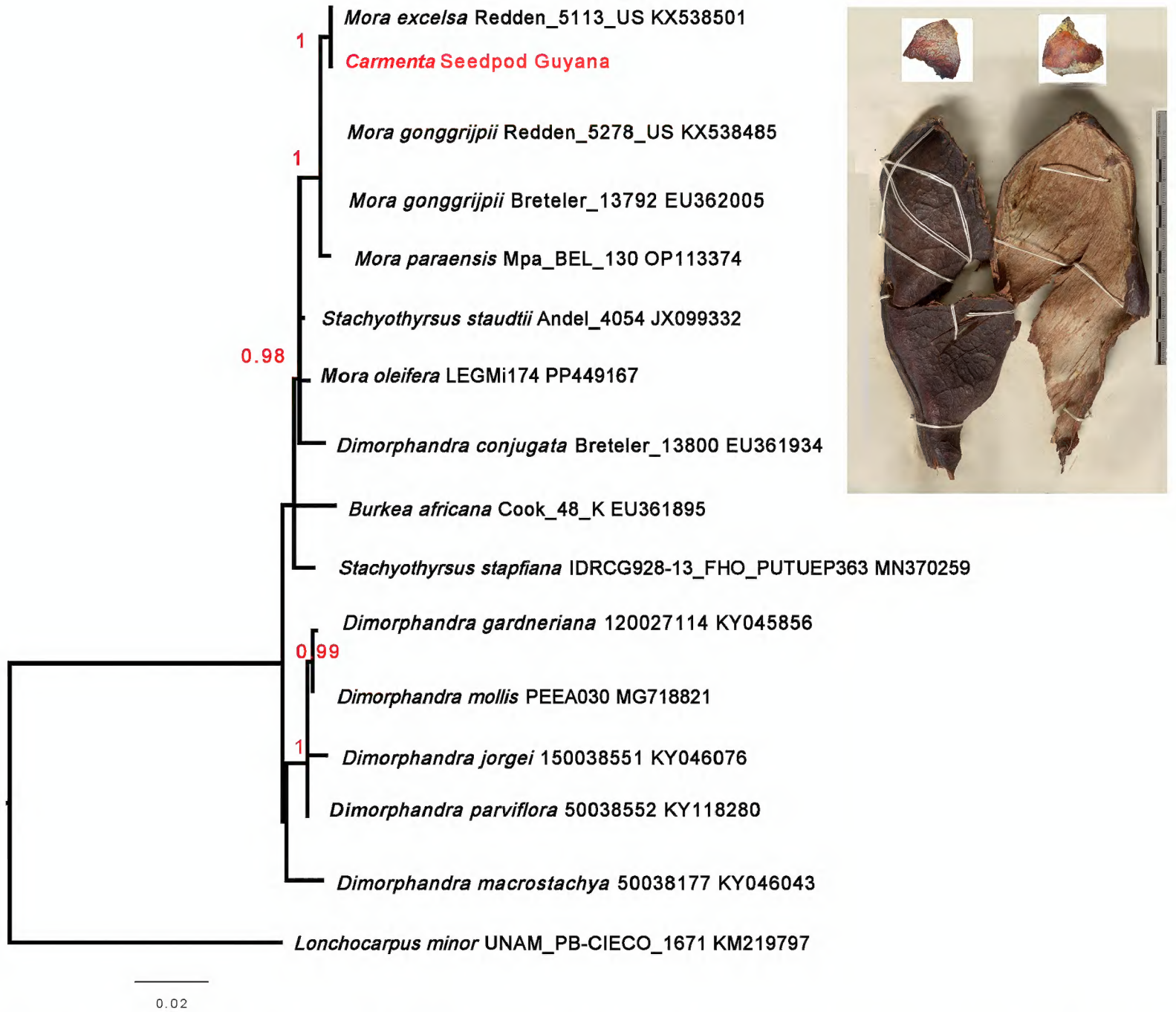

Figure 9. Phylogenetic tree for the Matk marker using Phyml 3.0 and including a sequence of the seed-pod fragment (in red) and for of all genera found in the Bruneau et al. (2024) caesalpinioid phylogeny for their tribe Dimorphandreae, with representative species downloaded from GenBank (on 1/05/2024). Supports shown on nodes are via the ABayes measure in Phyml 3.0 (see Methods) with a minimum of 0.95 being considered significant for the purposes of this analysis. Both surfaces of the pod fragment are shown for scale (vertical, measuring 10 cm) in the context of herbarium sample USNM 11469 (http://n2t.net/ark:/65665/m3e49b8ed5-5042-44f1-8892-5e4217055c5f) for the seed pods of a *M. excelsa* specimen from Trinidad and Tobago. There is an exact match with *M. excelsa* for this marker.

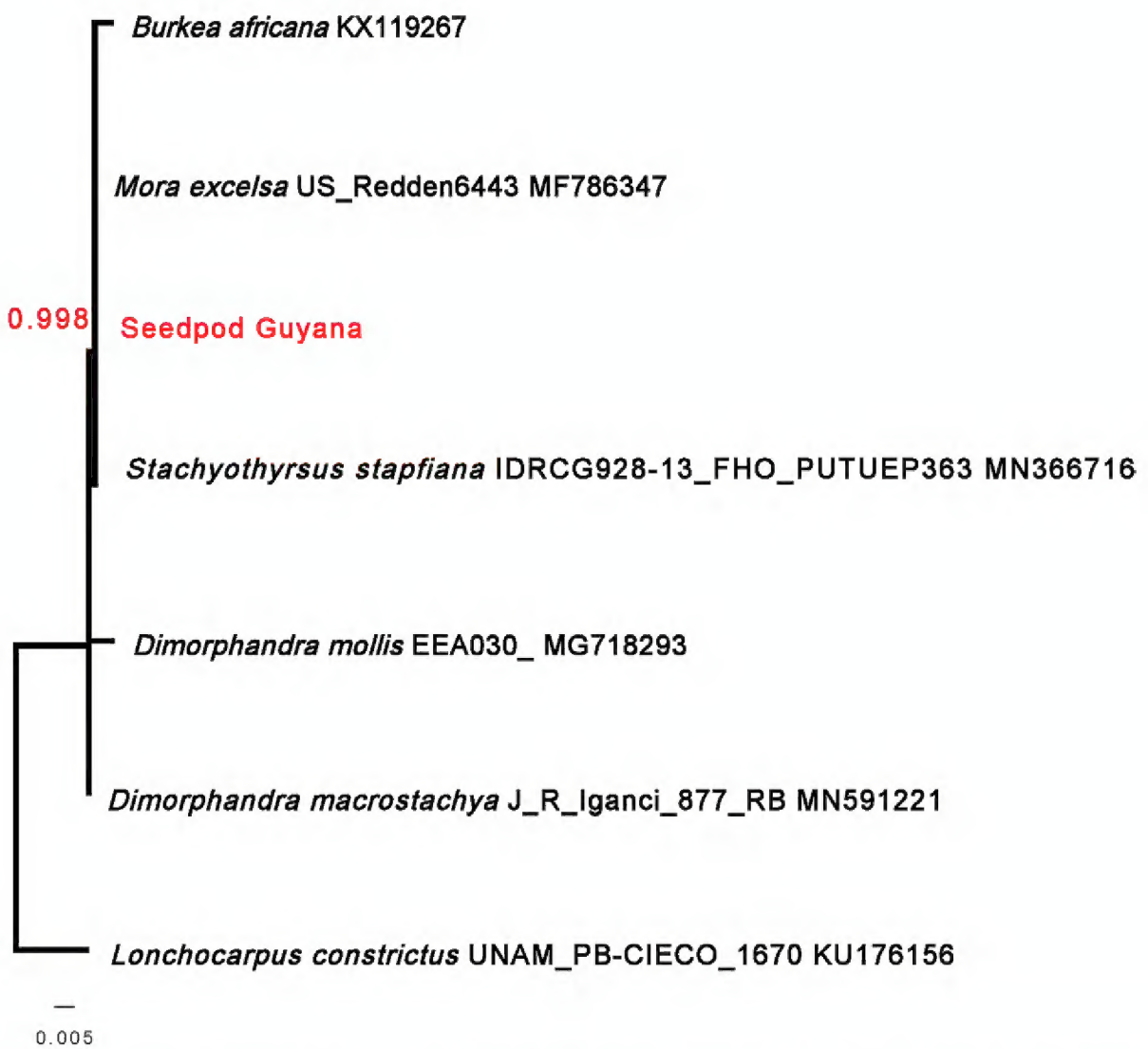

Figure 10. Phylogenetic tree for the rbcL marker including sequences of the seedpod fragment (in red) and of all genera found in the Bruneau et al. (2024) caesalpinioid phylogeny for their tribe Dimorphandreae, with representative species downloaded from GenBank (on 1/05/2024). Supports shown on nodes are via the ABayes measure in Phyml 3.0 (see Methods) with a minimum of 0.95 being considered significant for the purposes of this analysis. The match is consistent with an identity of *M. excelsa* and representatives of two other genera for this marker.

The type(s) of *Sesia surinamensis* Möschler, 1878 are described as lost in Duckworth and Eichlin (1978) and are not figured in Arita et al. (2021). Following our enquiry, both Möschler's syntypes, a male and a female, were located by Théo Léger and Viola Richter in Museum für Naturkunde, Berlin, and we were therefore able to examine photographic images of both specimens. Both the male and the female differ in external appearance from the mystery clearwing. Additionally, the barcodes for the two specimens from Surinam identified on BOLD as *C. surinamensis* which were supplied to BOLD by the Sesiidae Research Group (one from the Research Collection of Franz Pühringer) that fall in the BIN BOLD:AAK2798 were 8.17–8.87% divergent from the DNA barcode of the mystery clearwing.

For *Carmenta benoisti* and *C. flavostrigata* there are substantial differences between photographic images of the types and the drawings of those types on the one hand and the unknown specimens on the other.

C. theobromae is, as mentioned above, a pest species on Cacao. Although we have not been able to review an image of the type specimen, the mystery clearwing specimens are different in physical appearance from the non-type specimen in the NHMUK collection and the images we have reviewed in the pest literature and various other sources. As stated above, DNA barcode data show confusion between *C. surinamensis*, *C. theobromae*, and *C. foraseminis*, so identities in the pest literature should be taken with caution.

Morphological systematics

Carmenta brachyclados Sterling & Lees, sp. nov.

https://zoobank.org/44BD181A-79A6-4153-A1CB-DFDC4C5D4238

Type material. ***Holotype*** • ♀, wingspan 18 mm, fwl 8 mm, Central Guyana, ex seedpod fragment *Mora excelsa* (det. DNA barcode), accidentally collected ca. 12.x.2023 (leg. Ashleigh Cadet) and transported to United Kingdom, adult found live indoors, Wales, Neath, Port Talbot, 04.ii.2024, leg. Daisy T. Cadet, specimen number NHMUK013700462, accession number BMNH(E) 2024-18. ***Paratype*** • ♀ same collection data as holotype except found dead in house, specimen number NHMUK013700463, slide number NHMUK014332461. The types have been deposited at the NHMUK (see also Associated material not individually linked to each type).

Barcode index number. BOLD:AGA4441.

Diagnosis. Hindwing with branch of M_3 and CuA_1 very short ($1/10^{th}$ of distance between edge of discal cell and termen), forewing with discal spot narrow and tapering below M_3 towards dorsum, exterior transparent area elongate, with moderately convex outer margin, apical area predominantly black, reaching close to branch of R_4 and R_5, entire area between stalks of R_4 and R_5 scaled black (Figs 11–13). Similar to *C. whitelyi* (See Similar species) but differs in length of branch of M_3 and CuA_1 in hindwing and in shape of discal spot and exterior transparent area (Figs 13, 14). Female genitalia with sclerotised section of ductus bursae long and thin, ductus seminalis arising at juncture of sclerotised and membranous section of ductus bursae (Fig. 15).

Description. Female (Figs 11–13). Wingspan 18–19 mm. ***Head.*** Frons dark yellow medially, laterally white, vertex metallic blue-black, patagium sulphur yellow; labial palps with all segments sulphur yellow, third segment tipped black; pilifers small, bristled; haustellum fully developed; antenna clavate, scape yellow, flagellum black with yellow reflections, apical scale tuft present. ***Thorax.*** Black with two longitudinal yellow stripes laterally and small medial yellow patch, tegulae black; foreleg with femur sulphur yellow, tibia blackish ventrally, sulphur yellow dorsally, tarsus sulphur yellow speckled with black; mid leg with femur and tibia black anteriorly, sulphur yellow posteriorly, tarsus sulphur yellow speckled blackish; hind leg with femur sulphur yellow, tibia black anteriorly, sulphur yellow posteriorly, tarsus sulphur yellow with black patch medially, posteriorly speckled black dorsally. ***Wings.*** Dorsally: Forewing with posterior transparent area tinged pale yellow, terminating under discal spot, line of sulphur yellow scales on dorsum from base to discal spot, discal spot narrow, straight, tapering below M_3 towards dorsum, exterior transparent area elongate, outer margin moderately convex, apical area almost extending to base of stalk of R_4 and R_5, black flecked with yellow scales, remaining area between apical area and base of stalk of R_4 and R_5 black, yellow scaling at base of M_1 and M_2, costa black with yellow reflections in some lights; hindwing with line of sulphur yellow scales on costa from base to beyond ¾, discal cross vein pale, branch of M_3 and CuA_1 very short ($1/10^{th}$ of distance between edge of discal cell and termen). Ventrally: Forewing as dorsal surface except costa yellow towards base and with substantial yellow scaling to discal spot, yellow scaling medially on outer margin of discal spot and extending some distance along M_1 and M_2, apical area with more yellow scaling than on dorsal surface. ***Abdomen.*** Dorsally black-blue with a narrow sulphur yellow ring posteriorly on each segment, anal tuft blue-black, edged yellow; ventrally sulphur yellow throughout, anal tuft darker yellow (Figs 1, 11, 12); pre-genital abdomen with apodemes scythe shaped, venulae short, broad, S8 with a pair of lateral crescent-shaped sclerites (Fig. 16).

Male. Unknown.

Female genitalia (Fig. 15). Papillae anales narrow, somewhat elongate; apophyses posteriores approximately the same length as apophyses anteriores; ostium narrow, slightly concave; sclerotised section of ductus bursae substantially longer than membranous section, constricted posteriorly, otherwise long, narrow, of even width throughout; ductus seminalis arising at juncture of sclerotised and membranous sections of ductus bursae; corpus bursae small and membranous, without signum.

Early stages. Two larval tunnels filled with a mixture of frass and silk were found between the two lignified surfaces of a fragment of seed pod of the leguminous tree *Mora excelsa* Benth. The pupal exuviae of one of the specimens is illustrated at Figs 2, 3. The larval workings and exit holes are illustrated at Figs 5, 6.

Distribution. Central Guyana. Accidentally transported to UK without release in the wild.

Etymology. The specific name is derived from brachys (gr.) short; klados (gr.) a branch. The species is named after the characteristic short branch of M_3 and CuA_1 in the hindwing.

Associated material. Hostplant voucher (*Mora excelsa* pod fragments): NHMUK013700486. Pupal exuviae of *Carmenta brachyclados* females: NHMUK013700484, NHMUK013700485 (these were not readily matchable to specific types and so have separate object numbers).

Similar species

A comparison of data on similar species of *Carmenta* to *C. brachyclados* is available in Suppl. material 1.

The closest taxa to *C. brachyclados* are *C. whitelyi* and a taxon we refer to (without describing) in this paper as *C.* cf. *whitelyi*. However, in *C. whitelyi* the branch of M_3 and CuA_1 in the hindwing is longer (1/5 distance between the edge of the discal cell and the termen) whereas in *C. brachyclados* it is shorter ($1/10^{th}$ of the distance between the edge of the discal cell and the termen). Also, in the forewing of *C. whitelyi*, the discal spot is broader and hardly tapers towards the dorsum and the exterior transparent area is subquadrate and comparatively narrow, with an almost straight outer margin, whereas in *C. brachyclados*, the discal spot is narrower and tapering below M_3 towards the dorsum, the exterior transparent area is elongate, and its outer margin is strongly convex (Figs 13, 14).

In *C.* cf. *whitelyi* the branch of M_3 and CuA_1 in the hindwing is a similar length to that of *C. whitelyi*, the discal spot is broader than in either *C. brachyclados* or *C. whitelyi* and the exterior transparent area is elongate, with the outer margin less convex than *C. brachyclados* (see Suppl. material 1).

The NHMUK collection has 5♂ and 12♀ which we have identified as *C.* cf. *whitelyi*, including eight specimens collected by Herbert Simpson Parish on 29.vi.1901. Existing DNA barcodes and other similar material in the NHMUK collection, including a large number of Le Cerf manuscript types, indicate that there is a complex group of similar species, and that this taxon is best described as part of a comprehensive review of that group.

Discussion

Type locality

The updated ICZN Code states that the type locality of a nominal species-group taxon is the geographical place of capture, collection or observation of the name-bearing type (Article 76.1). However, if capture or collection occurred after transport by artificial means, the type locality is the place from which the name-bearing type began its unnatural journey (Article 76.1.1) and this is our case. DNA analysis of the adults and the plant fragment, together with timing of emergence compared to

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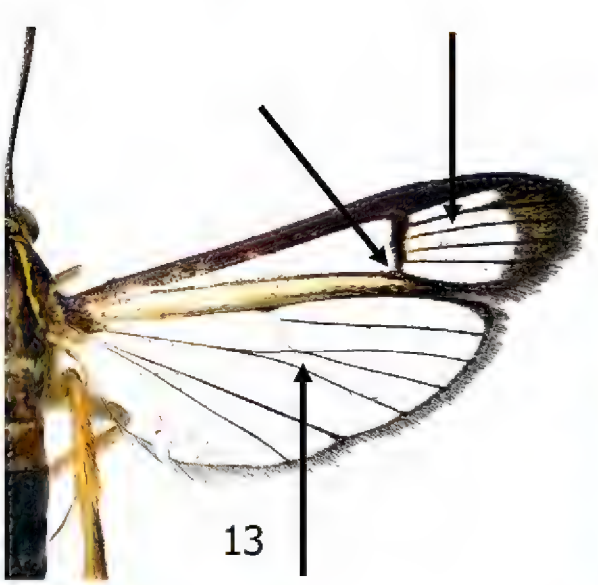

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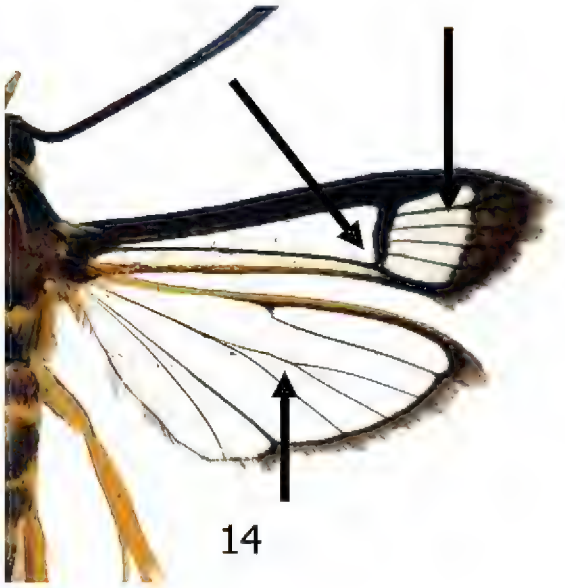

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Figures 11–16. *Carmenta brachyclados* sp. nov.; **11.** Holotype ♀ dorsal; **12.** Holotype ♀ ventral; **13.** External diagnostic characters of *C. brachyclados*; **14.** External diagnostic characters of *C. whitelyi*; **15.** Paratype of *C. brachyclados* ♀ genitalia slide number NHMUK014332461; **16.** Paratype of *C. brachyclados* pre-genital abdomen. Scale bars: 10 mm (**11, 12, 16**); 1 mm (**15**).

Ashleigh's work itinerary, point to the origin of the holotype in Guyana although the exact location is unclear. Aside from some savannah sites unlikely to constitute localities for *Mora excelsa* within the upper Rio Takuto, Tapunini and Upper Demerara - Berbice regions, Ashleigh's work in Guyana took her to a number of other sites in Upper Essequibo and Potaro-Siparuni. The Essequibo and Siparuni Rivers border the Iwokrama forest and Turtle Mountain range, sites that she visited, and she photographed a few large buttresses that might belong to *M. excelsa* near Iwokrama River Lodge on 12/10/2023. These regions are in the central part of Guyana (Fig. 17). Accordingly, we consider that the type locality is properly described as Central Guyana, rather than a broader area. *Mora excelsa* is a dominant, large buttress-rooted tree of riverine forest in the above localities, in contrast to *M. gonggrijpii*, which is characteristic of slopes and hilly terrain (Polak 1992). Although the adult specimens were found, one alive, in South Wales, they emerged indoors with none released in the wild and the species would anyway not be capable of establishing itself there.

Seed feeding habits

Fig. 2 shows that *C. brachyclados* is related to a group of clearwing moths, the described species of which include *C. foraseminis*, *C. surinamensis*, and *C. guyanensis*. Our results are consistent with those of Taft and Cognato (2017), who showed (their Fig. 1) that these three species

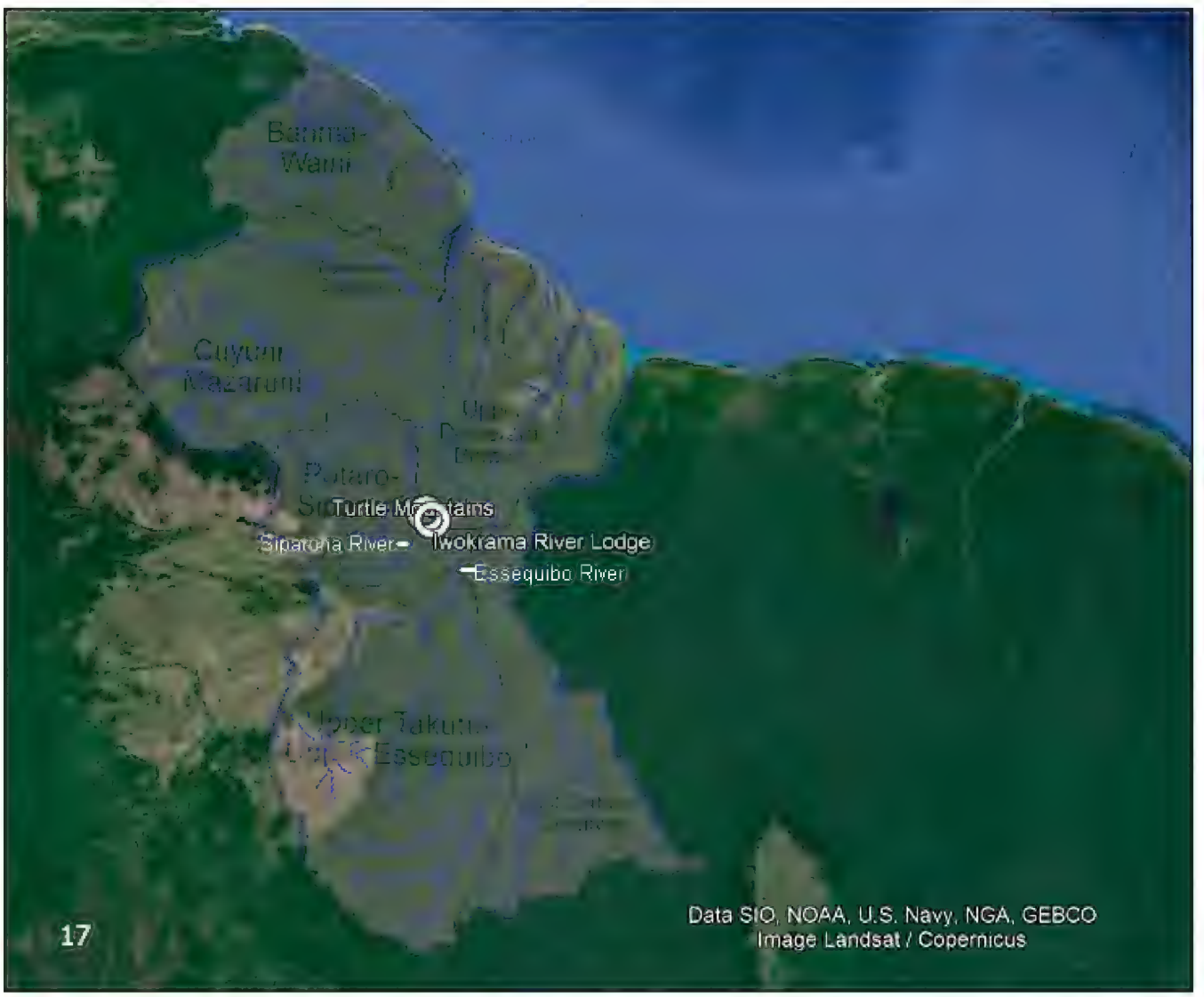

Figure 17. Map of Guyana showing the most likely sampling positions (white circles: Turtle Mountains and Iwokrama Forest/Iwokrama River Lodge) for the seedpod of *Mora excelsa* with the two live pupae of *Carmenta brachyclados* inside. Credit: Google Earth/Landsat/Copernicus/Rivers_Guyana.mkl/Guyana regions english.png (CC by 2.5).

form a clade, with the first two species being sisters in their study. *C. foraseminis* is known to feed within the fruits and seeds of *Gustavia superba*, the original specimens having been reared from fruits and seeds that were collected on the ground (Eichlin 1995; Harms and Aiello 1995); data online at BOLD also includes DNA barcoded specimens that were reared from *Lafoensia punicifolia*. *C. foraseminis* has also been recorded from seeds of *G. angustifolia* Benth., and a species of *Eschweilera* (Lecythidaceae), as well as from pods of cacao (*Theobroma cacao* L., Sterculiaceae). *C. surinamensis* is known to feed on seeds of *Pentaclethra* sp. and *Mora* sp. (both Fabaceae) and has also been identified as a species reared from *Prioria copaifera* Griseb. (Fabaceae) (Harms and Aiello 1995). The type of *C. theobromae* was bred from dry pods of cacao (Busck 1910) (note that sequences of the BIN BOLD:AAK2798 identified as *C. theobromae* as well as *C. foraseminis* from Peru on BOLD are likely to represent, however, *C. surinamensis*). Harms and Aiello also report undescribed species of clearwing as bred from fruits and seeds in the neotropics (Harms and Aiello 1995).

Harms and Aiello comment that, given that many, perhaps most, fruits and seeds are eaten by ground-foraging mammals (e.g., agoutis, squirrels, and peccaries) soon after falling, one would expect that individuals remaining in fallen fruit soon would be eaten or buried by mammals (Harms and Aiello 1995).

The fragment of seedpod we have examined shows that the larva of *C. brachyclados*, at least in its latter stages, bores between the hardened surfaces of the seed pod. This part of the pod will be less nutritious than the fruits or seeds but perhaps this is a defensive adaptation against predation by small seed and fruit-feeding mammals. It would be interesting to explore whether this or other similar species feed in fruits and/or seeds in the early stages of their development but transfer to the hardened part of seedpods, for better protection against predation, in the latter part of their development. There are other potentially significant roles of seed boring sesiids in the ecology of tropical forests. We do not know what happened to the seed(s) contained within this pod (*M. excelsa* pods have only 1–2 seeds: Polak 1992), but there are high chances that even damaged seeds can often sprout. Dalling et al. (1997), in a study of sprouting, found that seeds of *P. copaifera* and *G. superba* were both highly tolerant to such damage. The same phenomenon seems to be true of *M. excelsa*, if not more so. In a study of the antifeedant effects on *Spodoptera frugiperda* L. of the seeds of five Neotropical trees, those of *M. excelsa* from Guyana and Trinidad were found to be the most well defended (Bovell et al. 2019). Seed defence and survival is thought to be an important factor in this species forming monospecific stands (where it occupies as much as 85–95% of canopy abundance in Trinidad). It could be that an additional advantage of the strategy we infer for *C. brachyclados* is to avoid these antifeedants without necessarily affecting seeding germination rates.

Diversity of *Carmenta*

The genus *Carmenta* is exceptionally diverse, and there must be other undescribed species ready to discover in the Neotropics particularly (Taft and Cognato 2017). At a generic level the *Carmenta* assemblage is also phenotypically diverse and phylogenetically polyphyletic. Not only the genera previously stated but *Aegerina* Le Cerf, 1917 and *Euryphrissa* Butler, 1874 fall within *Carmenta* (F. Pühringer, pers. comm.). Also Cognato et al. (2022) were unable to establish a firm sister relationship between *Carmenta* and *Synanthedon* Hübner, [1819], leaving the possibility that the latter is paraphyletic with respect to *Carmenta*. *Synanthedon* however appears monophyletic if the Ethiopian (Africa south of Sahara) and Neotropical (America south of Mexico) species are

excluded from *Synanthedon* and only a few Palearctic and Oriental species are transferred to other genera (F. Pühringer, pers. comm.). These indications highlight the need for a much more comprehensive phylogenetic revision.

Conclusion

It is rare for a species of micromoth and most unusual for a species of larger moth (as that term is commonly used in the UK) to be newly described from specimens found in the UK. The last time the latter occurred was with *Thera britannica* (Turner, 1925).

However, the increase in the prevalence of international travel, both for work and leisure purposes, increases the likelihood of potentially interesting and important data on the biodiversity of insect species being found in somewhat unlikely places (Roques et al. 2010). The finding of this accidentally introduced species is an excellent example of how a piece of community science, assisted by social media, can lead to the capture and preservation of such data and increase our knowledge of the world's biodiversity.

Finally, prior to the development of pheromone lures, clearwing moths were notoriously difficult to find or rear, even by experienced lepidopterists (Zukowsky 1913: 1215). The chances of two clearwing moths from the Neotropics successfully emerging in South Wales, over three months after they arrived, from a small fragment of a seedpod of a tropical tree, accidentally stuck to the boot of a professional photographer, carried halfway round the world in a boot bag to a cold Welsh winter, and being preserved in good condition, together with their food source and pupal exuviae, seem highly remote. The jungle spirits were clearly with Ashleigh. It must have been very good tobacco.

Acknowledgements

We are grateful to Ashleigh Cadet for her patience in answering questions about the details of her work in Guyana. Many thanks also to Claire Griffin, Sequencing Assistant at the Natural History Museum London for her help in cryogenic grinding of seed material and providing the CTAB extraction protocol. We thank Dr. Sandra Knapp (NHMUK) for identifying the plant fragment as a piece of seedpod likely to belong to *Mora* sp. We thank Jacek Wajer (NHMUK) for kindly providing links to herbarium samples showing pods of *M. excelsa*. Théo Léger and Viola Richter of Museum für Naturkunde, Berlin are thanked for locating and photographing the syntypes of *Sesia surinamensis* Möschler, 1878. We are grateful to Dr Franz Pühringer for all his help, including permission to use the sequences for *Carmenta guyanensis* and *C. surinamensis* (Fig. 2), and his comments on and additional information for the paper. We also thank Graeme Davis and Les Evans-Hill for their role in the discovery of this species and our colleague, Sir Anthony Galsworthy, for his review of the manuscript and Dr Daniel Bartsch of the Naturkunde Museum Stuttgart for permission to include images of the types of *Synanthedon benoisti* and *S. flavostrigata* in our Suppl. materials 1, 2. Finally, we thank Dr Jadranka Rota, our subject editor and Dr Axel Kallies and Dr Marta Skowron, our other peer reviewers, for their helpful comments.

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Supplementary material 1

Supplementary table S1 and figures S1–S20

Authors: Mark J. Sterling, Daisy T. Cadet, Jordan Beasley, David C. Lees

Data type: pdf

Explanatory note: Comparison of data on similar species of *Carmenta* to *C. brachyclados*.

Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.

Link: https://doi.org/10.3897/nl.47.130138.suppl1

Supplementary material 2

Supplementary table S2

Authors: Mark J. Sterling, Daisy T. Cadet, Jordan Beasley, David C. Lees

Data type: xls

Explanatory note: Accession numbers and other data for sequences used in Figs 7–10.

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Link: https://doi.org/10.3897/nl.47.130138.suppl2